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Distribution of Antibiotic Resistance Genes in *Salmonella* spp. in Africa: A Systematic Review

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ABSTRACT

Antimicrobial resistance associated with *Salmonella* spp. represents a major global public health concern. In Africa, this challenge is particularly critical, as *Salmonella* spp. are a leading cause of foodborne diseases and act as significant reservoirs for the dissemination of antibiotic resistance genes (ARGs). This systematic review synthesizes data from studies published between 2013 and 2023 regarding the continental distribution of ARGs in *Salmonella* spp. across Africa. Publications were retrieved from PubMed, Scopus, and Google Scholar using predefined inclusion and exclusion criteria related to publication period, geographic location, and relevance to antibiotic resistance genes in *Salmonella* spp. Data were analyzed to evaluate the distribution of resistance genes across sample types (human, animal, food, and environmental sources), detection methods, geographic regions, and temporal trends. North Africa contributed the majority of studies (27; 43.5%), followed by West Africa (19; 30.6%), Southern Africa (9; 14.5%), East Africa (6; 9.7%), and Central Africa (3; 4.8%). Polymerase chain reaction (PCR) was the predominant method for detecting resistance genes, employed in 48 studies (77.4%). In contrast, quantitative PCR (qPCR) and whole-genome sequencing were used in 2 (3.2%) and 12 (19.4%) studies, respectively. Based on the frequency of occurrence across the included publications, the most frequently reported resistance genes were *blaTEM* (11.37%), *tetA* (7.78%), *blaCTX-M* (7.58%), *sul1* (5.83%), *sul2* (4.90%), *dfrA* (4.37%), and *qnrB* (3.79%). Overall, the findings highlight a broad diversity and widespread distribution of antibiotic resistance genes in *Salmonella* spp. across Africa. The frequent association of these genes with mobile genetic elements underscores the potential for horizontal gene transfer and the emergence of multidrug-resistant strains. These results demonstrated an urgent need for strengthened surveillance systems and the implementation of integrated One Health strategies linking human, animal, and environmental health sectors to mitigate antimicrobial resistance in African countries.

Keywords: Africa, Antibiotic resistance gene, One Health, Public health, *Salmonella* spp.

INTRODUCTION

Antibiotic resistance constitutes a major global public health challenge, escalating largely due to the widespread use in human and animal populations (McEwen and Collignon, 2018). While antibiotics are essential for treating bacterial infections, the acquisition of resistance mechanisms allows bacteria to survive and proliferate despite treatment, thereby compromising therapeutic efficacy and increasing mortality. Although antimicrobial resistance is a worldwide threat, its impact is particularly severe in resource-limited regions. In Africa, antimicrobial resistance is estimated to cause 27.3 deaths per 100,000 inhabitants annually, underscoring the urgent need for improved surveillance and management strategies (WHO, 2016; Da et al., 2023).

Salmonella spp. is a primary cause of foodborne infections in both humans and numerous animal species. Beyond its pathogenicity, this organism plays a critical role in the dissemination of antimicrobial resistance by accumulating antibiotic resistance genes (ARGs; Gargano et al., 2021). The increasing prevalence of *Salmonella* spp., a gram-negative bacterium in the *Enterobacteriaceae* family, is concerning, as it causes salmonellosis, a complex infectious disease ranging from mild gastroenteritis to severe systemic infections (Elhadi, 2014). In the African context, the significant prevalence of *Salmonella* spp. highlights its pivotal role in the burden of foodborne diseases (Tadesse et al., 2018).

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The emergence of resistant strains has complicated clinical management, as resistance to conventional antimicrobial agents renders previously reliable therapeutic options ineffective (VT Nair et al., 2018). Furthermore, resistant *Salmonella* strains can facilitate the horizontal dissemination of resistance by exchanging genetic determinants with other bacterial populations via mobile genetic elements (Giuriatti et al., 2017).

Consequently, continuous surveillance is imperative to monitor the evolution of resistance trends and to inform health policies aimed at controlling the spread of antibiotic-resistant *Salmonella* (Giuriatti et al., 2017). Recent phylogenetic and bioinformatics studies have further highlighted the genetic diversity and antimicrobial resistance gene variability of *Salmonella enterica* isolates in Africa (Esserghini et al., 2024; Esserghini et al., 2025). By consolidating recent data and identifying emerging resistance trends, this study aimed to systematically review and synthesize published data on the distribution of antibiotic resistance genes in *Salmonella* spp. across Africa between 2013 and 2023.

MATERIALS AND METHODS

Search and retrieval strategy

The present study was conducted as a systematic review of published literature reporting antibiotic resistance genes in *Salmonella* spp. from African countries. A total of 62 eligible studies published between 2013 and 2023 were included; the publication year refers to the year of article publication and not necessarily the year of microbiological sample collection. A comprehensive literature search was performed in PubMed, Scopus, and Google Scholar databases using microbiological, resistance-related, and geographic keywords combined with Boolean operators. The following search string was applied ("*Salmonella*" OR "*Salmonella* spp.") AND ("antibiotic resistance genes" OR "ARGs") AND (Africa OR African countries OR Algeria OR Angola OR Benin OR Botswana OR Burkina Faso OR Burundi OR Cabo Verde OR Cameroon OR Central African Republic OR Chad OR Comoros OR Republic of Congo OR Democratic Republic of Congo OR Côte d'Ivoire OR Djibouti OR Egypt OR Equatorial Guinea OR Eritrea OR Ethiopia OR Gabon OR Gambia OR Ghana OR Guinea OR Guinea-Bissau OR Kenya OR Lesotho OR Liberia OR Libya OR Madagascar OR Malawi OR Mali OR Mauritania OR Mauritius OR Morocco OR Mozambique OR Namibia OR Niger OR Nigeria OR Rwanda OR São Tomé and Príncipe OR Senegal OR Seychelles OR Sierra Leone OR Somalia OR South Africa OR South Sudan OR Sudan OR Tanzania OR Togo OR Tunisia OR Uganda OR Zambia OR Zimbabwe). Records retrieved from the databases were screened based on predefined inclusion and exclusion criteria. Eligible studies reported *Salmonella* spp. isolated from human clinical samples (stool, blood, and urine), animal sources (poultry and livestock), food products (meat, eggs, milk, and seafood), and environmental samples (water and wastewater. As this review employed a descriptive synthesis approach, no statistical meta-analysis was undertaken, and data extraction was conducted at the study level to prevent double-counting of overlapping samples.

Data extraction

Data were systematically extracted from the full-text publications retrieved from scientific databases, using a standardized Microsoft Excel spreadsheet applied consistently throughout the review. Extracted variables included publication year, country, and African region, sample type (food, human, or environmental), methodological approaches for bacterial identification and antibiotic resistance gene detection, and specific resistance genes reported in each study.

Due to heterogeneity in study design and reporting practices, data on sample size, isolate numbers, and resistance gene prevalence were inconsistently available and therefore excluded from synthesis. Each publication received a unique reference identifier ensuring traceability.

Inclusion and exclusion criteria

Inclusion criteria encompassed original research articles published in peer-reviewed English-language journals between 2013 and 2023, focusing exclusively on *Salmonella* spp. studies conducted in African countries. Exclusion criteria eliminated studies conducted outside Africa, publications beyond the specified timeframe, review articles, commentaries, editorials, conference abstracts, articles not addressing antibiotic resistance genes, studies with insufficient antibiotic resistance genes data, non-English publications, and investigations focusing solely on non-*Salmonella* pathogens.

RESULTS

Study selection methodology

The methodological diagram outlines the approach used to assess the study selection process (Figure 1). Database searches in PubMed, Google Scholar, and Scopus initially identified 1,890 records. Following title and abstract screening, 1,100 records were excluded, with an additional 80 duplicates removed. Subsequently, 710 full-text articles underwent eligibility assessment. Among these, 648 articles were excluded for specific reasons, including publication outside the predefined study period (n = 370), absence of antibiotic resistance genes data (n = 220), insufficient data on resistance genes (n = 50), and non -English language (n = 8).

Ultimately, 62 articles were included and categorized by African region. The distribution showed a predominance of studies from North Africa with 27 articles (43.54%), followed by West Africa (19 articles, 30.64%), Southern Africa (9 articles, 14.51%), East Africa (6 articles, 9.7%), and Central Africa (3 articles, 4.83%).

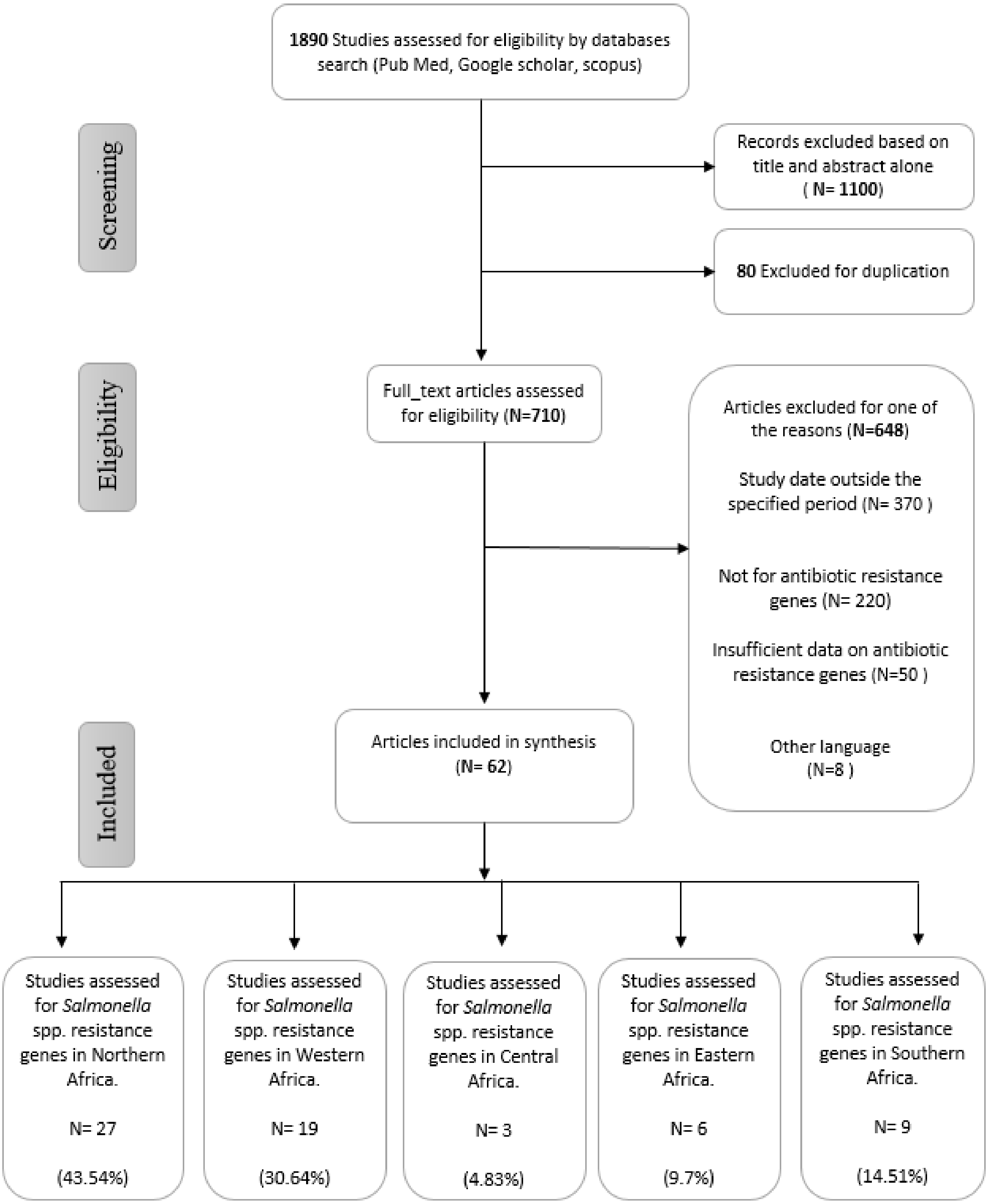

Figure 1. Flow diagram of the study inclusion process

Bacterial characterization and antimicrobial resistance assessment strategies

This systematic review, which included 62 published studies, demonstrated extensive application of conventional culture-based and biochemical methods for *Salmonella* spp. isolation, with several employing matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS).

Phenotypic antimicrobial susceptibility testing exhibited methodological variability; many studies utilized agar disk diffusion method according to the Kirby–Bauer protocol, while others proceeded directly to molecular analyses without phenotypic testing. Regarding genotypic approaches, 48 studies (77.41%) employed polymerase chain reaction (PCR) for the detection of resistance genes, two studies (3.22%) utilized quantitative PCR (qPCR), and 12 studies (19.48%) applied whole-genome sequencing (WGS) for comprehensive antimicrobial resistance profile characterization (Figure 2).

Figure 3 illustrates the distribution of antibiotic resistance genes in *Salmonella* spp. across African countries. Among the 54 African countries, only a limited subset contributed to publications during the study period. Egypt produced the highest number (14 publications), followed by Nigeria (13) and Tunisia (8). Other countries, including South Africa, Burkina Faso, Algeria, Morocco, Zimbabwe, Libya, Senegal, and others, contributed one to six publications each. A substantial proportion of African nations reported minimal or no publications, indicating marked geographic disparities in scientific output.

Figure 4 presents the annual publication distribution reporting antibiotic resistance genes in *Salmonella* spp. from 2013 to 2023. An overall increasing trend characterized publication output over time. The years 2019, 2021, 2022, and 2023 exhibited elevated publication numbers (5, 10, 14, and 15 publications, respectively). In contrast, a decrease in publication numbers was observed in 2020, which may be associated with disruptions in scientific research activities during the COVID-19 pandemic. Collectively, figures 3 and 4 highlight pronounced geographic disparities in scientific productivity and temporal fluctuations in publication activity during the study period.

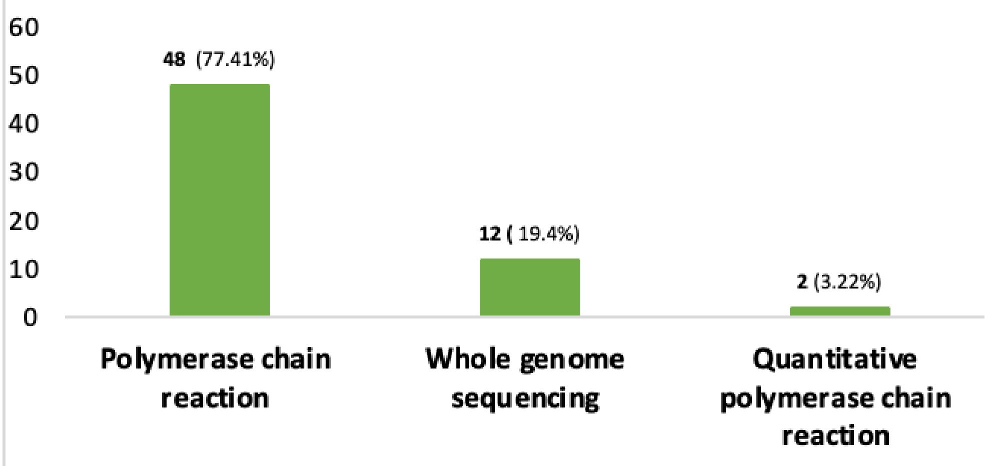

Figure 2. Molecular methods used for detecting antibiotic resistance genes in *Salmonella* spp.

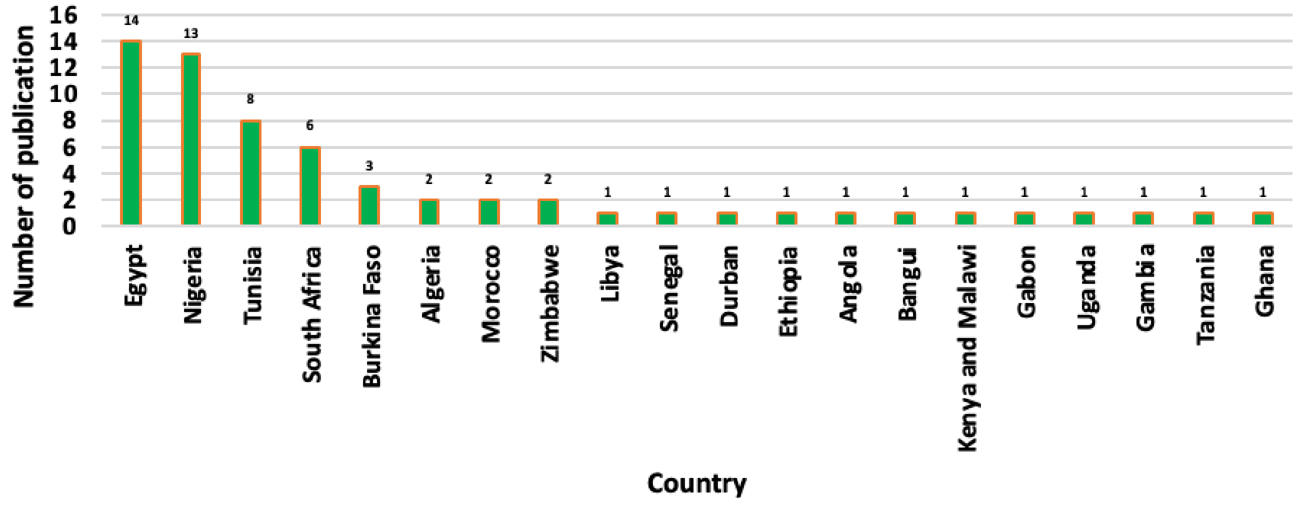

Figure 3. The included publications of resistance genes of *Salmonella* spp. in African countries during 2013-2023.

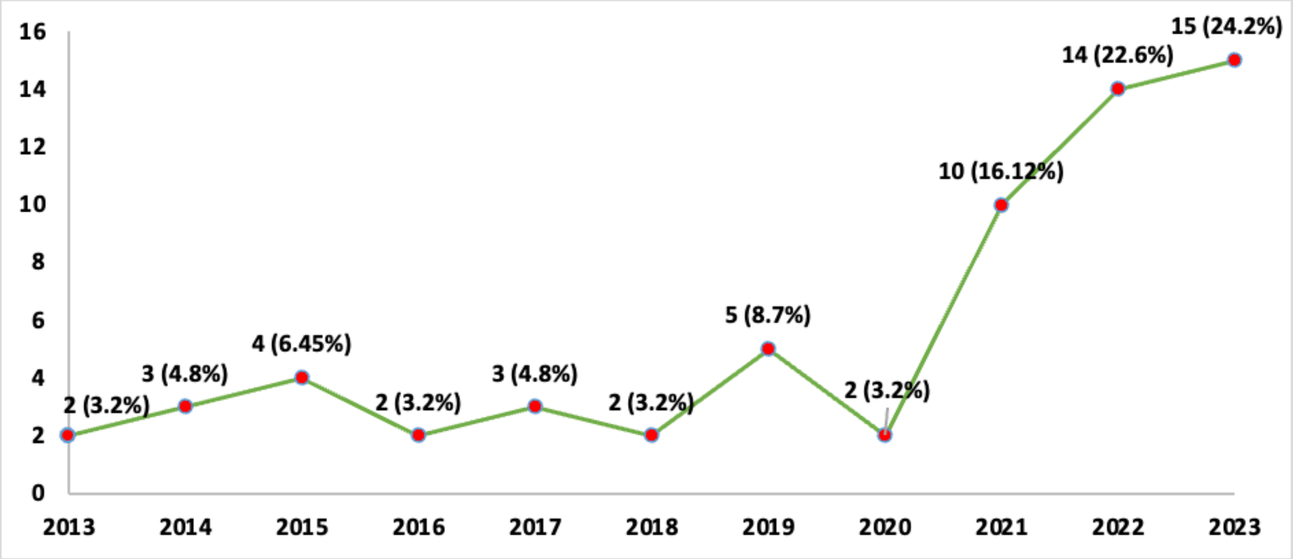

Figure 4. Annual number of publications on resistance genes of *Salmonella* spp. in African countries (2013-2023)

Study distribution by sample type

The distribution of articles and sample types collected in each country is detailed in Table 1. Articles concerning food samples constituted the majority, followed by those related to human samples, whereas articles focusing on environmental samples were the least numerous. In total, 50 articles involved food samples, 28 involved human samples, and 9 involved environmental samples. Some articles included multiple sample types, making it common to identify analyses of human, environmental, and food samples within the same publication.

As a result, the total number of articles for each sample type did not necessarily correspond to the overall number of included studies. This discrepancy was due to the inclusion of multiple sample types within a single publication. For instance, although 28 studies reported analyses of human samples, several of these studies also investigated food samples. As illustrated in Figure 5, studies involving food samples accounted for 58% of the total, followed by studies on human samples (32%) and environmental samples (10%).

Table 1. Country-level distribution of included studies by sample type in Africa (2013-2023).

Country	Number of articles	Number of articles by sample type			Reference
		Humans	Environments	Foods	
Egypt	14	3	1	13	Rushdy et al. (2013); Abdel-Maksoud et al. (2015); El-Sharkawy et al. (2017); Elhariri et al. (2020); Abou Elez et al. (2021); Adel et al. (2021); El-Aziz et al. (2021); Shalaby et al. (2022); Algammal et al. (2023); Diab et al. (2023); Ezzat et al. (2023); Fahmy et al. (2023); Omar et al. (2023); Shousha et al. (2023)
Nigeria	13	9	1	9	Abdullahi et al. (2014); Adesiji et al. (2014); Ajayi et al. (2019); Jibril et al. (2021); Ibrahim et al. (2022); Igbinosa et al. (2022); Ikhimiukor et al. (2022); Kamilu and Mukhtar (2022); Akinyemi et al. (2023); Fakorede et al. (2023); Jibril et al. (2023); Uzairue et al. (2023); Nwosu et al. (2023)
Tunisia	8	3	3	9	Al-Gallas et al. (2013); Hassena et al. (2021; 2022); Oueslati et al. (2021; 2022); Al-Gallas et al. (2022); Walid et al. (2023)
South Africa	6	1	1	5	Igbinosa (2015); Iwu et al. (2016); Jaja et al. (2019); Mthembu et al. (2019); Ramatla et al. (2019); Myataza et al. (2023)
Burkina Faso	3	-	1	2	Somda et al. (2021); Kagambèga et al. (2022); Soubeiga et al. (2022)
Algeria	2	1	1	3	Djeffal et al. (2017); Samia et al. (2021)
Morocco	2	1	1	2	Murgia et al. (2015); Ed-Dra et al. (2018)
Zimbabwe	2	2	-	1	Thilliez et al. (2022); Mashe et al. (2023)
Libya	1	1	-	-	Seiffert et al. (2014)
Senegal	1	1	-	-	Harrois et al. (2014)
Durban	1	1	-	1	Zishiri et al. (2016)
Ethiopia	1	1	-	1	Eguale et al. (2017)
Angola	1	1	-	-	Francisco et al. (2018)
Bangui	1	1	-	-	Breurec et al. (2019)
Kenya and Malawi	1	-	-	1	Wilson et al. (2020)
Gabon	1	1	-	-	Mabika Mabika et al. (2021)
Uganda	1		-	1	Onohuean and Igere (2022)
Gambia	1	1	-	-	Darboe et al. (2022)
Tanzania	1	-	-	1	Munuo et al. (2022)
Ghana	1	-	-	1	Archer et al. (2023)
Total	62	28	9	50	

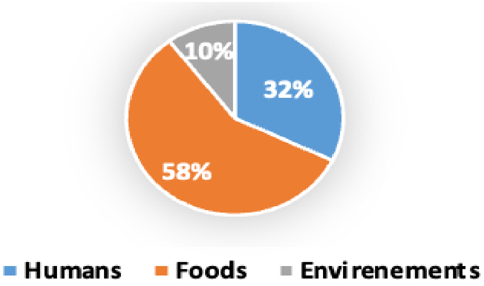

Figure 5. Proportional distribution of included studies by sample type in Africa (2013-2023).

Distribution of studies and antibiotic resistance genes of *Salmonella* spp. across different African countries

Figure 6 illustrates the study distribution and reported antibiotic resistance genes identified in *Salmonella* spp. across different African subregions over the period 2013-2023. Northern Africa exhibited the highest study concentration, particularly Egypt (27 studies), reflecting substantial regional research investment. This subregion also showed a relatively high number of reported antibiotic resistance genes (111). Western Africa yielded 19 studies reporting 127 cumulative resistance genes. Despite fewer studies (3), Central Africa reported 18 resistance genes. Eastern Africa comprised six studies reporting 39 resistance genes, while Southern Africa contributed nine studies with a total of 45 reported resistance genes. Overall, the distribution highlighted marked regional variation in both the study distribution and the cumulative number of antibiotic resistance genes reported in *Salmonella* spp. across Africa.

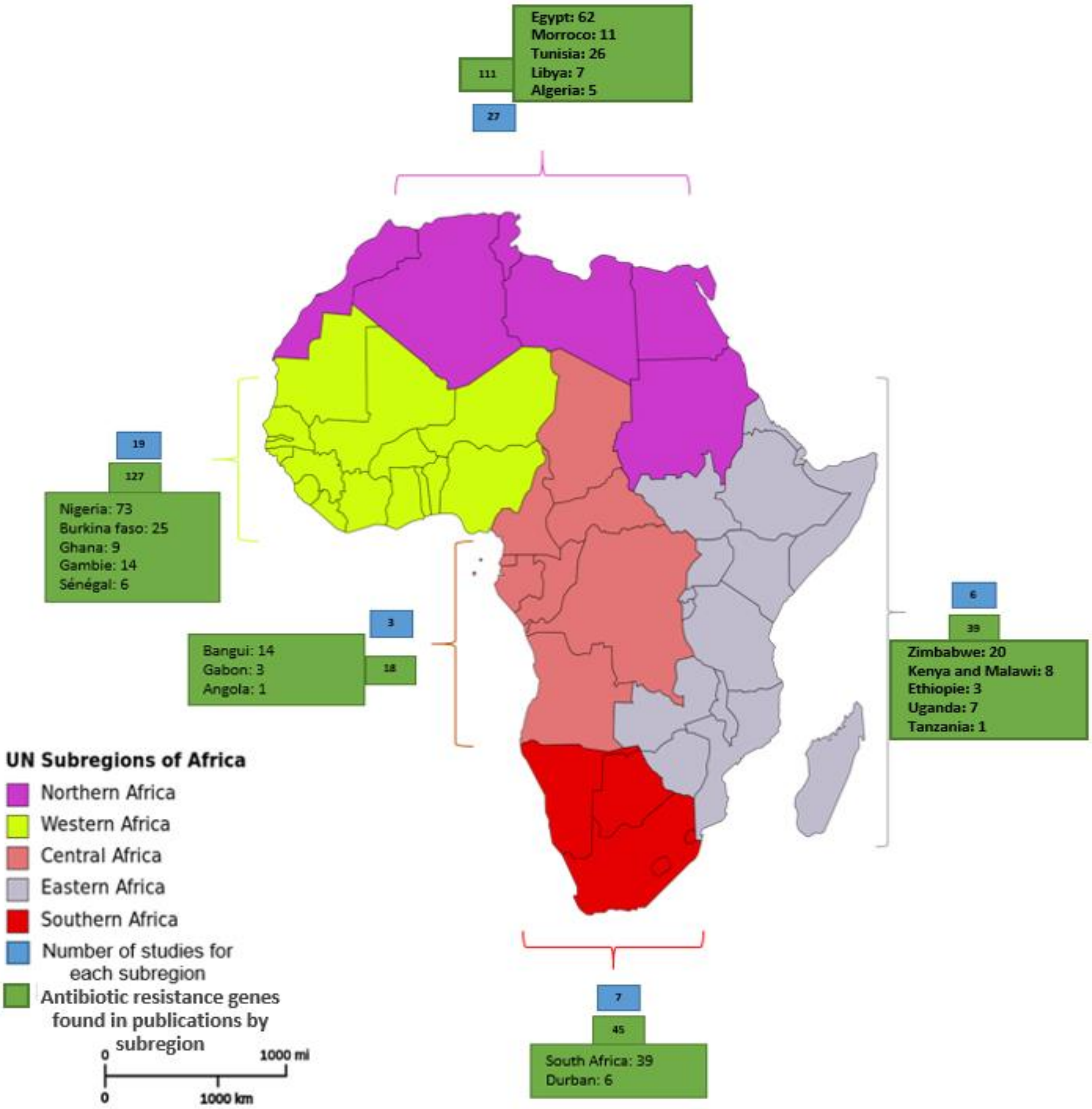

Figure 6. The distribution of studies and antibiotic resistance genes of *Salmonella spp.* found in publications across different subregions of the African continent

Distribution of studies reporting antibiotic resistance genes in *Salmonella* spp.

The distribution of publications reporting antibiotic resistance genes in *Salmonella* spp. over a ten-year study period (2013-2023) revealed a clear temporal pattern, with 2022 exhibiting the highest diversity of reported resistance genes, accounting for 23.28% of the total observed. In 2022, a marked increase was observed, with 81 antibiotic resistance genes reported across various studies, representing a substantial increase compared with previous years. The years 2014, 2015, and 2019 also demonstrated relatively high levels of reported resistance genes, with 24, 21, and 50 genes, respectively, while 2018 and 2020 exhibited relatively low proportions (2 and 13 genes). These findings underscored the temporal evolution of antibiotic resistance in *Salmonella* spp., as documented in scientific publications, and emphasized the importance of continuous surveillance activities to further characterize and monitor this phenomenon. Figure 7 illustrates the annual counts of reported antibiotic resistance genes based on published studies and does not represent a modeled prevalence of resistance genes over time.

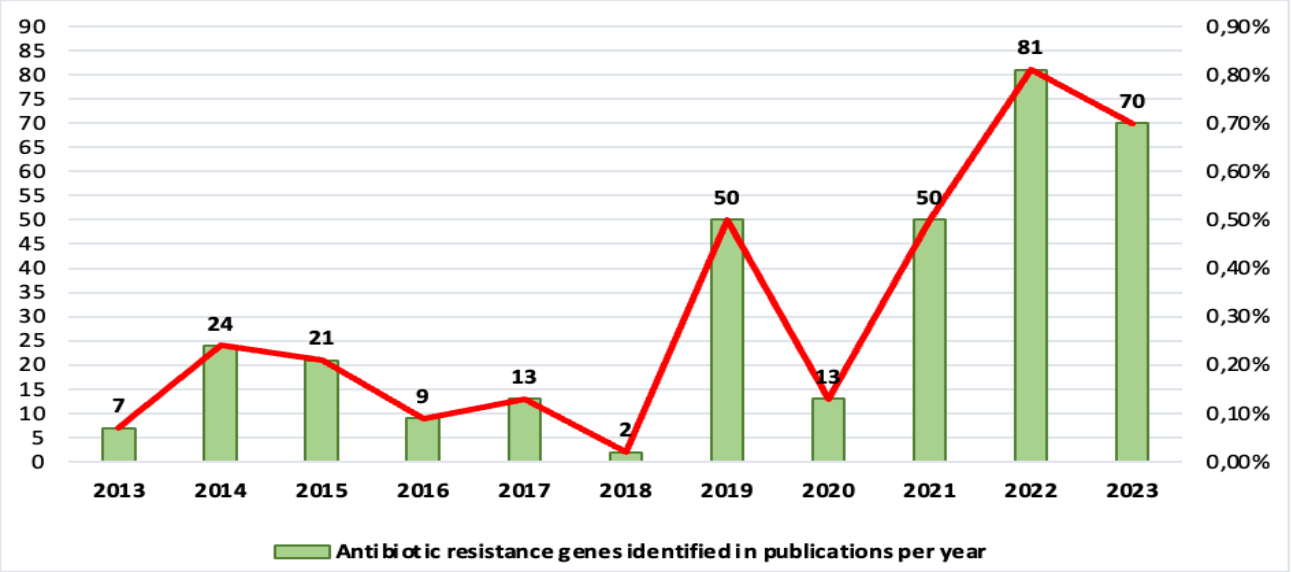

Figure 7. Temporal evolution of antibiotic resistance genes reported in studies on *Salmonella* spp. in African countries (2013-2023)

Antibiotic resistance profile of identified genes

Table 2 presents a comprehensive profile of antibiotic resistance genes identified in *Salmonella* spp. isolates across included studies. For beta-lactams, several resistance genes were reported, including *VEB-8*, *blaZ*, *blaCMY*, *blaSHV*, *blaTEM*, *blaCTX*, *blaOXA*, and *Blapse-1*. For cephalosporins, the genes *CMY-4*, *Cm1A*, *Cm1B*, and *ramA* were identified. Multiple resistance genes for aminoglycosides, such as *aphA*, *aph(3'')-1b*, *aph(6)-1d*, *aad(A)*, *qeqA*, *ant(3'')-IA*, *aac(3)-Ia*, and *aac(6')-Ib-cR*, were also reported. Other antibiotic classes, such as tetracyclines, macrolides, fosfomycins, chloramphenicol, quinolones, sulfonamides, and trimethoprim, were associated with specific resistance genes. For quinolones, resistance was primarily linked to point mutations in genes such as *gyrA*, *gyrB*, *parC*, and *parE*, which were associated with resistance, rather than the genes themselves. The reported isolates originated from different African countries, as summarized in Table 1.

Table 2. The spectrum of antimicrobial resistance genes of *Salmonella* spp. has been reported in studies conducted across African countries

Antimicrobial class	Resistance genes or mutations
Beta-lactams	*VEB-8, blaZ, blaCMY, blaSHV, blaTEM, blaCTX, blaOXA, Blapse-1*
Cephalosporins	*CMY-4, Cm1A, Cm1B, ramA*
Aminoglycosides	*aphA, aph(3'')-1b, aph(6)-1d, aad(A), qeqA, ant(3'')-IA, aac(3)-Ia, aac(6')-Ib-cR*
Tetracyclines	*tetA, tetB, tetD, tetK, tetJ, tet(X4), tetM*
Macrolides	*mphA, ereA, eremC, tmrB*
Fosfomycins	*FosA, FosA7-1, FosB*
Chloramphenicol	*floR, cat, Ph (3)11a*
Quinolones	Mutations: *gyrA, gyrB, parC, parE* Genes: *qnrA, qnrB, qnrS, oqxB, mdfA*
Sulfonamides	*Sul1, Sul2, Sul3*
Trimethoprim	*dfrA*
Streptogramins	*strA, strB*
Rifampicin	*rpoB*

Distribution of antibiotic resistance gene occurrences in *Salmonella* spp. in Africa based on publications (2013-2023)

The analysis of Table 3 indicated that several resistance genes, notably *blaTEM* (40 occurrences, or 11.37%), *tetA* (27 occurrences, or 7.78%), *blaCTX-M* (25 occurrences, or 7.58%), *sul1* (20 occurrences, or 5.83%), *sul2* (17 occurrences, or 4.90%), *dfrA* (15 occurrences, or 4.37%), and *qnrB* (13 occurrences, or 3.79%), were frequently reported in African publications on *Salmonella* spp. from 2013 to 2023. These genes, associated with resistance to beta-lactams, tetracyclines, sulfonamides, and dihydrofolate reductase inhibitors, highlighted important resistance mechanisms in the region, with implications for infection management. A temporal increase was observed between 2020 and 2023, particularly for *tetA* and *sul1*, which may have reflected increased antibiotic usage or improved surveillance. Additionally, genes such as *gyrA*, *parC*, *parE*, and *gyrB*, while not direct resistance genes, were included due to point mutations conferring quinolone resistance rather than representing direct resistance genes. Overall, the literature-derived resistance gene distribution highlights critical priorities for antibiotic surveillance and resistance management throughout Africa.

Table 3. Annual distribution of antimicrobial resistance genes detected in *Salmonella* spp. isolates reported in publications from African countries (2013-2023).

Antibiotic resistance genes detected in *Salmonella* spp.	**Gene classification**		**Year**											
	Direct resistance genes	**Genes with mutations associated with resistance**	**2013**	**2014**	**2015**	**2016**	**2017**	**2018**	**2019**	**2020**	**2021**	**2022**	**2023**	**Total over 10 years**
blaTEM	∨		-	-	4	-	3	1	5	2	4	14	7	40
tetA	∨		-	2	1	2	1	-	4	-	5	6	6	27
blaCTX	∨		-	1	-	-	3	-	1	-	8	5	7	25
Sul1	∨		-	2	2	1	1	1	3	-	2	5	3	20
Sul2	∨		-	1	2	1	-	-	3	2	1	7	-	17
dfrA	∨		-	-	-	-	-	-	2	-	1	9	3	15
qnrB	∨		1	1	-	-	-	-	1	-	4	1	5	13
aph(3'')-1b	∨		-	-	-	-	-	-	-	1	-	8	3	12
aad(A)	∨		-	-	1	-	-	-	3	-	2	3	3	12
Cat	∨		-	-	1	-	1	-	5	1	-	3	1	12
blaSHV	∨		-	2	1	-	-	-	-	1	1	4	2	11
aac(3)-Ia	∨		-	1	1	-	-	-	2	-	2	1	4	11
tetB	∨		-	1	-	1	-	-	1	-	2	4	1	10
blaOXA	∨		-	1		-	1	-	2	1	1	1	3	10
qnrS	∨		1	-	-	-	-	-	1	-	4	1	2	9
gyrA		∨	1	-	1	-	-	-	-	1	3	1	1	8
qnrA	∨		1	1	-	-	-	-	1	-	1	-	4	8
strA	∨		-	-	1	1	-	-	2	-	-	2	-	6
aac(6')-Ib-cR	∨		1	2	-	-	-	-	1	-	-	2	-	6
blaCMY	∨		-	-	-	-	-	-	1	1	1	-	2	5
Sul3	∨		-	1	-	-	1	-	-		1	-	1	4
aph(6)-1d	∨		-	-	-	-	-	-	-	1	-	-	3	4
ampC	∨		-	-	1	1	-	-	1	1	-	-	-	4
floR	∨		-	-	1	-	1	-	-	-	-	1	1	4
tetC	∨		-	1	-	-	1	-	2	-	-	-	-	4
mphA	∨		-	1	-	-	-	-	-	-	-	2	-	3
Blapse-1	∨		-	-	2	1	-	-	-	-	-	-	-	3
tetG	∨		-	1		-	-	-	-	-	-	-	1	2
FosB	∨		-	-	-	-	-	-	-	-	-	-	2	2
tetM	∨		-	-	-	-	-	-	1	-	1	-	-	2
aphA	∨		-	-	-	-	-	-	2	-	-	-	-	2
Cm1A	∨		-	1	-	-	-	-	1	-	-	-	-	2
gyrB		∨	-	-	1	-	-	-	-	-	1	-	-	2
qeqA	∨		1	-	-	-	-	-	-	-	1	-	-	2
parC		∨	1	-	1	-	-	-	-	-	-	-	-	2
rpoB	∨		-	-	-	-	-	-	-	-	-	-	1	1
eremC	∨		-	-	-	-	-	-	-	-	-	-	1	1
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mdfA	√		-	-	-	-	-	-	-	-	-	-	1	1
FosA	√		-	-	-	-	-	-	-	-	-	-	1	1
FosA7-1	√		-	-	-	-	-	-	-	-	-	1	-	1
oqxb	√		-	-	-	-	-	-	-	-	1	-	-	1
ramA	√		-	-	-	-	-	-	-	-	1	-	-	1
tet(X4)	√		-	-	-	-	-	-	-	-	1	-	-	1
parE	√	√	-	-	-	-	-	-	-	-	1	-	-	1
tetJ	√		-	-	-	-	-	-	-	1	-	-	-	1
tmrB	√		-	-	-	-	-	-	1	-	-	-	-	1
tetK	√		-	-	-	-	-	-	1	-	-	-	-	1
tetD	√		-	-	-	-	-	-	1	-	-	-	-	1
blaZ	√		-	-	-	-	-	-	1	-	-	-	-	1
strB	√		-	-	-	-	-	-	1	-	-	-	-	1
Ant (3'')-IA	√		-	-	-	1	-	-	-	-	-	-	-	1
Ph (3)11a	√		-	1	-	-	-	-	-	-	-	-	-	1
Cm1B	√		-	1	-	-	-	-	-	-	-	-	-	1
CMY-4	√		-	1	-	-	-	-	-	-	-	-	-	1
VEB-8	√		-	1	-	-	-	-	-	-	-	-	-	1
Total: 56	52	4	7	24	21	9	13	2	50	13	50	81	70	340

DISCUSSION

Salmonella spp. cause an estimated 93 million gastroenteritis cases and 155,000 deaths annually worldwide (WHO, 2016). Antimicrobial therapy the cornerstone of salmonellosis management; however, the increasing emergence of antimicrobial resistance has become a major public health concern, driven largely by the extensive antibiotics use in human medicine and animal production (Eshrati et al., 2025). Current projections suggest that antibiotic-resistant pathogens could cause 10 million deaths annually by 2050 if present trends persist. Consequently, the World Health Organization has emphasized the urgent necessityg for transitioning toward enhanced antimicrobial stewardship and robust global surveillance frameworks (Castro-Vargas et al., 2020).

This systematic review covered the period from 2013 to 2023 and included 62 eligible publications from African countries, adopting a structured and descriptive approach to synthesize findings regarding *Salmonella* spp. identification and characterization and associated antibiotic resistance genes.

Polymerase chain reaction has been widely used as a molecular technique for identifying antibiotic resistance genes (van Hoek et al., 2005). This detection method offers several advantages, including simplicity, rapidity, and high reproducibility. By employing specific primers targeting known DNA sequences, PCR enables reliable and accurate identification of antibiotic resistance genes in *Salmonella* spp. isolates (Abdel-Maksoud et al., 2015). The current study's findings highlight the extensive use of PCR in *Salmonella* spp. antimicrobial resistance research, with approximately 77.41% (48/62) of examined studies employing this molecular approach, demonstrating its efficacy and methodological suitability of PCR for routine identification of antibiotic resistance genes in *Salmonella* spp. Conversely, qPCR also presents significant advantages for antibiotic resistance gene detection, enabling precise, rapid target gene identification with quantification capabilities for both relative and absolute microorganism levels. However, q-PCR requires more sophisticated equipment and incurs higher reagent costs compared with standard PCR. Despite these advantages, qPCR remains underutilized in *Salmonella* spp. resistance studies (Galhano et al., 2021). Descriptive analysis of the included studies showed that only 3.22% (2/62) employed qPCR for resistance gene detection, indicating that this technique remains underutilized and may warrant broader application in future investigations of antimicrobial resistance.

In contrast, 19.4% (12/62), of studies utilized whole genome sequencing for more comprehensive analysis. These findings align with previous studies, which showed that the majority of studies (15 out of 18) detected antibiotic resistance genes using PCR, while five studies employed WGS. However, the preference for standard PCR underscores its effectiveness in the specific and rapid detection of resistance genes, which is essential for understanding and monitoring the evolution of antibiotic resistance in *Salmonella* spp (Abdel-Maksoud et al., 2015). Thus, standard PCR remains a valuable tool for combating the spread of antibiotic resistance and for guiding strategies to prevent and treat antibiotic-resistant *Salmonella* infections (Galhano et al., 2021).

The observed results regarding antibiotic resistance genes in *Salmonella* spp. in African countries highlight the distribution of articles by sample type and country of origin. The majority of studies focused on food-related samples, accounting for 58% of the total samples analyzed. Human samples constituted the second most frequent sample type at 32%, while environmental samples were the least collected at 10%. These findings are consistent with a study conducted by (El Hanafi et al., 2023) which also reported that the percentage of samples from food products was 61.9%, human samples were 28.6%, and environmental samples were 14.3%. This sample types distribution underscores the importance of elucidating *Salmonella* transmission pathways and the prevalence of antibiotic resistance genes across different epidemiological contexts, particularly in food- and human-associated settings.

West African countries confront serious emerging antibiotic resistance challenges comparable to those in other global regions. This phenomenon is exacerbated by various factors related to underdevelopment, such as unfavorable socio-economic conditions, lack of qualified human resources, and insufficient infrastructure for diagnosing and evaluating antibiotic resistance. Additionally, across several West African countries, absence of national and regional antimicrobial resistance surveillance networks, coupled with inappropriate use and unsecured circulation of antibiotics, contributes to the spread of resistance. Furthermore, the variable quality and availability of antibiotics, together with the widespread antimicrobial agent use in livestock production systems, promote the emergence and dissemination of antibiotic resistance genes (Ouedraogo et al., 2017).

These factors partially explain the significant increase in detected antibiotic resistance genes in the present systematic review in West Africa, where 127 resistance genes were reported, compared to other African subregions. Specifically, North Africa reported 111 genes, Central Africa 18 genes, East Africa 39 genes, and Southern Africa 45 genes. Furthermore, the synthesis of published studies on *Salmonella* spp. resistance in Africa indicates that, among 54 African countries, only 21 have been represented by eligible studies, including Egypt (14 studies), Nigeria (13 studies), Tunisia (8 studies), South Africa (6 studies), Burkina Faso (3 studies), while the remaining countries were represented by limited publications.

Notably, no eligible publications were identified for 33 of the 54 African countries included in this review, indicating substantial geographic gaps in published data on antibiotic resistance genes in *Salmonella* spp. across these regions. Regarding the number of publications per year, there is an overall increasing trend over the years. The years 2019, 2021, 2022, and 2023 exhibited elevated publication output (5, 10, 14, and 15 articles, respectively). Conversely, 2020 publication numbers declined, likely attributable to the impact of the COVID-19 pandemic on scientific research and article publication in this field (Raynaud et al., 2021).

Antibiotic resistance genes distribution reported in *Salmonella* spp. across African studies published between 2013 and 2023, indicated specific resistance determinant predominance. Extended-spectrum β-lactamase genes, particularly *blaTEM*, were frequently reported, suggesting sustained selective pressure from β-lactam use in both clinical and agricultural contexts. Resistance genes associated with tetracyclines (*tet*) and sulfonamides (*sul1* and *sul2*) were also commonly identified, reflecting the extensive and long-term use of these antimicrobial classes in food-producing animals. Although plasmid-mediated quinolone resistance genes (*qnrB*) exhibited lower reporting frequencies, their detection remains epidemiologically relevant due to their role in horizontal gene transfer and multidrug resistance dissemination. Comparable resistance patterns have been described in large-scale genomic studies, including a global analysis of *Salmonella* spanning the period 1900-2023, which identified antimicrobial usage, host reservoirs, and environmental factors as key drivers of resistance evolution (Wang et al., 2025). Similarly, national genomic surveillance in China demonstrated that temporal trends in antimicrobial resistance were shaped by socio-environmental and epidemiological factors (Wang et al., 2023). These findings suggest that analogous drivers may contribute to observed African resistance patterns, highlighting the importance of integrated, region-specific surveillance strategies.

β-lactamases are bacterial enzymes, particularly Gram-negative bacteria, that confer resistance to β-lactam antibiotics. Among *Salmonella* spp. studies, the presence of the *blaTEM* gene is well documented (Maka and Popowska, 2016), notably in Vietnam, where it was predominant among ampicillin-resistant retail beef strains (Thai et al., 2012), as well as in Canada, where it was detected in retail meat isolates (Aslam et al., 2012). These findings illuminate β-lactamase gene diversity in *Salmonella* spp. and their role in antimicrobial resistance roles.

The *blaCTX* gene is a critical β-lactamase gene associated with antibiotic resistance in Gram-negative bacteria, including *Salmonella* spp. Studies have identified *blaCTX* in *Salmonella* isolates, highlighting its role in resistance to critical antibiotics. For example, *blaCTX-M-1* detection in German ceftiofur-resistant *Salmonella* isolates emphasizes the significance of β-lactam resistance (Rodríguez et al., 2009). Understanding the specific prevalence of the *blaCTX* gene in *Salmonella* spp. is essential for effective antimicrobial management (Rodríguez et al., 2009).

The *tetA* gene, associated with tetracycline resistance in *Salmonella* spp., is frequently detected in antibiotic resistance studies (Gargano et al., 2021). It belongs to a gene class mediating tetracycline resistance, often residing in mobile genetic elements such as plasmids or transposons (Aldema et al., 1996). Studies have identified *tetA* in *Salmonella* strains isolated from animals and food samples, highlighting its role in the dissemination of resistance (Gargano et al., 2021). For instance, *tetA* was detected in 14 out of 25 (56%) tetracycline-resistant strains and was prevalent among animals in close contact with humans (Aldema et al., 1996).

The genes *sul1* and *sul2* mediate sulfonamide resistance in *Salmonella* spp. (Sköld, 2000). Typically, plasmids located; these genes encode dihydropteroate synthase (DHPS) variants unaffected by sulfonamides. Studies have shown that these genes are widely spread among sulfonamide-resistant *Salmonella* spp. Isolates (Sköld, 2000). For example, a study conducted in Vietnam on *Salmonella* spp. isolates from beef samples found sulfonamide resistance in 39.7% of isolates (25/63), among which 80.0% (20/25) were positive for the *sul1* gene (Thai et al., 2012). Similarly, a Canadian study of retail meat (chicken, turkey, and pork) *Salmonella* isolates showed 71% sulfonamide resistance , with *sul1* detected in 5 isolates and the *sul2* gene in 3 isolates (Aslam et al., 2012).

The *dfrA* gene is associated with trimethoprim resistance in *Salmonella* spp (Chen et al., 2004). This gene encodes dihydrofolate reductase (DHFR) variants with reduced trimethoprim affinity, enabling bacteria in its presence. Studies have shown that trimethoprim-resistant isolates of *Salmonella* spp. often carry *dfrA* genes, which are a key mechanism of resistance to this antibiotic (Chen et al., 2004).

The gene *qnrB*, a plasmid-mediated quinolone resistance determinant (PMQR) found in *Salmonella* spp., confers resistance by protecting the target site against antimicrobial agents binding (Karczmarczyk et al., 2010). Studies have identified various *qnrB* gene variants in *Salmonella* isolates from diverse sources (Karczmarczyk et al., 2010).

CONCLUSION

This systematic review provides a descriptive synthesis of published studies on the distribution of antibiotic resistance genes in *Salmonella* spp. across Africa at the continental level from 2013 to 2023, revealed a broad diversity and widespread dissemination of genes conferring resistance to specific types of antibiotics, including *blaTEM*, *tetA*, *blaCTX*, *sul1*, *sul2*, *dfrA*, and *qnrB*. *Salmonella* spp. were frequently reported as important carriers of these resistance genes, contributing to the emergence of multidrug-resistant strains. *Salmonella* spp. genetic adaptability facilitates the dissemination of resistance genes, which are frequently associated with mobile genetic elements, including plasmids. Addressing this public health challenge requires an integrated One Health framework that links the human, animal, and environmental health sectors. Such approaches, combined with robust epidemiological investigations, can elucidate critical pathways of antibiotic resistance gene transmission. Implementing comprehensive One Health strategies is imperative for developing effective policies to combat antimicrobial resistance and safeguard public health.

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Authors’ contributions

Hajar Esserghini and Dhaud Odei Ansong participated in data collection and verification. Hajar Esserghini conducted the literature search and prepared the original draft of the manuscript in consultation with Adnane Benmoussa and Nadia Ziyate. Najib Al Idrissi and Hassan Ghazal contributed to data interpretation and participated in manuscript revision. Salsabil Hamdi and Fadil Bakkali contributed to the design and implementation of the study, the analysis of the results, and the critical revision of the manuscript. All authors checked and approved the final edition of the manuscript for publication in this journal.

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Ethical considerations

The authors declare that this manuscript is original and is not being considered elsewhere for publication. Ethical issues, including consent to publish, misconduct, data fabrication, and redundancy, have been checked by all authors. The authors did not use any AI tools for writing and preparing this article.

Availability of data and materials

All data generated or analyzed during this study are included in this article.

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